

Please amend the paragraph found on page 4, line 11 to page 5, line 1, amended by preliminary amendment, as follows. Applicants have attached a copy of the marked-up paragraph on a separate page, with deletions and additions to the text indicated by bracketing and underlining, respectively.

b2 One key methodology is described by Sahin, et al., Proc. Natl. Acad. Sci. USA 92: 11810-11913 (1995), incorporated by reference. Also, see U.S. Patent 5,698,396 and 6,025,191. All three of these references are incorporated by reference. To summarize, the method involves the expression of cDNA libraries in a prokaryotic host. (The libraries are secured from a tumor sample). The expressed libraries are then immunoscreened with absorbed and diluted sera, in order to detect those antigens which elicit high titer humoral responses. This methodology is known as the SEREX method ("Serological identification of antigens by Recombinant Expression Cloning"). The methodology has been employed to confirm expression of previously identified tumor associated antigens, as well as to detect new ones. See the above referenced patents and Sahin, et al., supra, as well as Crew, et al., EMBO J. 14: 2333-2340 (1995).

In the Claims

Please amend the claims as follows. Applicants have attached a copy of the marked-up claim on a separate page, with deletions and additions to the text indicated by bracketing and underlining, respectively.

b3 6.(twice amended) An isolated protein encoded by an isolated nucleic acid molecule selected from the group consisting of:

(a) nucleic acid molecules which encode a cancer associated antigen, and which comprise a nucleotide sequence, the complementary sequence of which hybridizes, under stringent conditions, to at least one second nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of the nucleotide sequences set forth as SEQ ID NOS: 1, 2, 3, 4, and 5,

(b) nucleic acid molecules that differ from the nucleic acid molecules of (a) in codon sequence due to the degeneracy of the genetic code, and

(c) full length complements of (a) or (b).